

Amendments to the Specification:

*Please replace the title at page 1 with the following title:*

~~Crystal Structure of ACPS/ACP Complex, Solution Structure of B. Subtilis ACP, and~~  
~~Uses Thereof~~ Crystals of an Acyl Carrier Protein Synthase/Acyl Carrier Protein Complex

*Please replace the first paragraph on page 1 and as amended in the preliminary amendment filed with the application on November 19, 2003, with the following amended paragraph:*

This application is a divisional of U.S. Patent Application No. 09/770,834, filed January 25, 2001, now ~~allowed~~ U.S. Patent No. 6,684,162, which claims the benefit of U.S. Provisional Application No. 60/202,466, filed May 8, 2000, the contents of both of which are herewith incorporated by reference.

*Please replace the paragraph beginning at page 7, line 15, and amended in the preliminary amendment filed November 19, 2003, at page 6, with the following amended paragraph:*

~~Figure~~ Figures 3 and 3A-1 to 3A-79 ~~provides~~ provide the atomic structural coordinates for ACPS and ACP as derived by X-ray diffraction of an ACPS-ACP crystal. "Atom type" refers to the atom whose coordinates are being measured. "Residue" refers to the type of residue of which each measured atom is a part – i.e., amino acid, cofactor, ligand or solvent. The "x, y and z" coordinates indicate the Cartesian coordinates of each measured atom's location in the unit cell (Å). "Occ" indicates the occupancy factor. "B" indicates the "B-value", which is a measure of how mobile the atom is in the atomic structure (Å<sup>2</sup>). "MOL" indicates the segment identification used to uniquely identify each molecule. Under "MOL", "A1", "B1" and "C1" refers to each molecule of ACPS (SEQ ID NO:2), "AP1", "AP2" and "AP3" refers to each molecule of ACP (SEQ ID NO:1), and "W" refers to water molecules.

*Please replace the paragraph beginning at page 7, line 26, and amended in the preliminary amendment filed November 19, 2003, at page 7, with the following amended paragraph:*

Figure 4 represents the sequence alignment of *B. subtilis* ACP (SEQ ID NO:1), *E.coli* ACP (SEQ ID NO:15), and *Streptomyces coelicolor* A3(2) ACP (SEQ ID NO:16).

*Please replace the paragraph beginning at page 8, line 1, and amended in the preliminary amendment filed November 19, 2003, at page 7, with the following amended paragraph:*

~~Figure~~ Figures 5 and 5A-1 to 5A-15 ~~provides~~ provide the atomic structural coordinates for the restrained minimized mean structure of *B. subtilis* ACP (SEQ ID NO:1) as derived by NMR spectroscopy. "Atom type" refers to the atom whose coordinates are being measured. "Residue" refers to the type of residue of which each measured atom is a part – i.e., amino acid, cofactor, ligand or solvent. The "x, y and z" coordinates indicate the Cartesian coordinates of each measured atom's location (Å). The last column indicates the temperature factor field, representing the rms deviation of the 22 individual NMR structures about the restrained minimized mean structure. All non-protein atoms are listed as HETATM instead of atoms using PDB conventions.

*Please replace the abstract at page 52 with the following amended abstract:*

This ~~invention~~ disclosure is directed to the crystal structure of *Bacillus subtilis* (*B. subtilis*) Acyl Carrier Protein Synthase (ACPS) complexed with *B. subtilis* Acyl Carrier Protein (ACP), the solution structure of *B. subtilis* ACP, and to the use of these structures in rational drug design methods to identify agents that may interact with active sites of ACPS and ACP, and to the testing of these agents to identify agents that may represent novel antibiotics.